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OI IO IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 4_x_3_and_5.res made by spaula on Wed 4 Dec 102 14:37:04-PST.

Query sequence being compared:US-09-886-241-4 (1-1506)
   File : 886241-copy.seq
Number of sequences searched:          2
Number of scores above cutoff:         2
```

Results of the initial comparison of US-09-886-241-4 (1-1506) with:

```
N
U  50-
M     -
B     -
E     -
R     -
      -
O     -
F  10-
      -
S     -
E   5-
Q     -
U     -
E     -
N     -
C     -
E     -
S   0-------------------------------------------------------------------
        11    11    11    11    11    11    11    11    11    11         *
SCORE 01    14    12    16    21    25    29    33    37                 137
STDEV -9    -8    -7    -6    -5    -4    -3    -2    -1    0             1
```

```
                    PARAMETERS
      trity matrix     Unitary
      th penalty             1
Gap penalty              1.00    K-tuple              4
Gap size penalty         0.33    Joining penalty     30
Cutoff score                0    Window size        500
Randomization group         0
```

```
               SEARCH STATISTICS
           Mean    Median    Standard Deviation
Scores:     34       33            3.54

           CPU                 Total Elapsed
Times:  00:00:00.00            00:00:00.00

Number of residues:          2513
Number of sequences searched:   2
Number of scores above cutoff:  2
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name   Description   Length Init. Opt. Sig. Frame
                                                                              Score Score Score
----
1. US-09-886-241-3- Sequence 3, Application U   427   37   142   0.85   0
2. US-09-886-241-5- Sequence 5, Application U   2086   32   647 -0.57   0

1. US-09-886-241-4 (1-1506)
   US-09-886-241-3- Sequence 3, Application US/09886241

Initial Score   = 37   Optimized Score   =   142   Significance = 0.85
Residue Identity = 36   Matches   =   368   Mismatches   =   238
Gaps   =   2   Conservative Substitutions =   83   0

          740   750   760   770   780   790   800
CACCCAGCCTGCATCTCCCAGGAGGAAGTGGAGGGGACATGCTGTCCCCAGAAACCCACTCTATCCTCAC
                                                             ||| | |||
                                                        AAAAAAGAAAAAAATTCAA
                                                          x   10   20

    810   820   830   840   850   860   870
CCTGTTTGTTGCTCTTCCCCTGCCCTGCTAGGGCTGCGGCTTCTGACTTCTAGAAGACTAAGGCTGGTCTGT
|-||||||| || || ||| || || | || ||-----||--| |
CATTTTATTT--------------TG--AGAAAT----TTCAAAC--CTACAA---AAAGTTG--CAGG
     30   40   50   60

    880   890   900   910   920   930   940
GTTTCCTTGTTGTTGCCCACCTTGGCTG--ATACCCAGAGAGAACTCGGGCACTTGCTGCCTGATGCCCACCCCT
| | ||| ||||||||| ||| |-| ||| | ||| ||--| |-|--| |
AATAG--TGT--------CTAT--CTGAAATACATATTCAGTCTTTTCTTTAGAAG-NNNNNNNNNNNNNN
    70   80   90   100   110   120

    950   960   970   980   990   1000   1010   1020
GCCAGTCATTCCTCCATTCACCCAGCGGAGGTGGGATGTGAGCAGCAGCCCACCATTGGAAAATCCAGAAACC
                                                       |||||| ||
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTAAAATC-----ACT
    130   140   150   160   170   180

   1030   1040   1050   1060   1070   1080   1090
GGGAACAGGGATTGCCCTTCACAATTCTACTCCCCAGATCCTCTCCCCTGGACACAGCCCACAGGGC
|-|||||||||| ||| || ||| || ||||||| |||||||| |||||||||
GTGACCACTGACTT---AGCACA---TACT-----GGACCGTTGCTCCT-----AGGAGAAATACAGGGT
    190   200   210   220   230   240

   1100   1110   1120   1130   1140   1150   1160
AG-GACCCTAAGATCTGGGGAAAGGAGGTCCTGAGACACCTTGAGGTACCCTTAGATCCTTTTCTA-CCCACT
||-||||||| ||||||||| ||||||| ||||| | | ||| ||| | |||| || | | | || ||||
TTCGTTCCTGTGAGCTTTGCTCGTGATATTTCATCAGC-TGATCAATATGTA-ATCTTGTTTTATGTGTAT
    250   260   270   280   290   300   310

   1170   1180   1190   1200   1210   1220   1230
TTCCTATGGAGGATTCCAAGTCACCACTTCTCTCACCGGCTTCTACCAGGCTCCAGGACTAAGGCCTTTTC
|||-| ||||| | ||||| |||||| || | |||| ||| | | | ||| ||| |||||
TTCTGTTTAAAGATTC------NNNNNNNNNNNNNNNNNNNNNNNNNGTTGAGCTTGTTA-CCCTTGAAC
    320   330   340   350   360   370

   1240   1250   1260   1270   1280   1290   1300
TCCATAGCCTCAACATTTTGGAATCTTCCCTTAATCACCCTTGCTCTCCTGCTCCTCCTGGGGTGCCTGGAGATGGACT
| ||| | |||||| | ||||| | |||| ||||| ||| | |||| || | ||| |||
T-CACAGCC-CACAGGACTAGAACACATGCCTAAATAAAGTTTATCTAACAT
    380   390   400   410   420

   1310   1320   1330
GGCAGAGACCTCTTTGTTGCGTTTTGTGCT
```

2. US-09-886-241-4 (1-1506)
   US-09-886-241-5- Sequence 5, Application US/09886241

Initial Score     =  32    Optimized Score     =    647    Significance = -0.57
Residue Identity  =  47    Matches             =    300    Mismatches   =    825
Gaps              =        Conservative Substitutions =    300                0

4_x_3_and_5.res

```
                                                    x        10
                                     TAAATTCCGG--CCGCGT-CG
                                     ||| |||| || |||| | |
TTAAAGGATACCAGTTGGAATCTCTCTTTATTAATCACCAGAGAACCATGAACAACAAGCTGTTTATCATTTG
     120        130        140        150        160 x      170        180

  x        10                                       20
TAAATTCCGG--CCGCGT-CG                          ACGCAGCCTTACAGAGACTGGA---AAAGAAGCCCAAAC---CAAG--GCCCCCAGAGAGGTCCCCCAGGCC
||| |||| || |||| | |                           || ||| |||  |||  ||  |||   ||    | | ||| |||||||||||||| |||| |||||||
                                     ACTCATCATT---TAATCTTGAATTCCAGCTTCTCACACTTCTCACAGGAT
                                       190        200        210        220        230        240        250
```

[Alignment continues — dense nucleotide sequence alignment with position markers from ~120 through ~1780, including poly-A tail AAAAAAAA at the end]

4_x_3_and_5.res

```
||| || ||| |||        || || |||    |-|   ||||| |-|||-|| |||-|
CTTTCTTGTCTCTTAAATTACTTACTTCCTTGC----ACA---CTTTGCCATACAAGAATGAACATGAGCT
1790      1800      1810      1820         1830      1840      1850

TTTCTTGTGTAGATCTGAGTTGAAATCCTGTGGACACTGGGCGAAT
1860      1870      1880      1890
```